

HUMAN TELOMERASE

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCGAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCCCGCCGCCCCCTCCTCCGCGAGGTGTCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTTACCACCAGCGTGCGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCAGCTGCGCGCTCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCGCGCGCTGTACCAGCTCGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCGGGGGGAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240

FIG. 1A

GGCGCTGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCACCCGGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCAGTCCCTGGGACACGCCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCGGTGTACGCGGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGCAATGCCAGGGACTCCCCGAGGTTGCCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGCTGGTGCCCCAGGCCTCTGGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500

FIG. 1B

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AS ORIGINALLY FILED

GCCPAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC	1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC	1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
TTTTATGTACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTC	1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
TGGAGCAAGTTGCAAAGCATTGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGGAG	1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAGCCAGGCCCGCCCTGCTGACGTCCAGA	1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCGGATTGTGAACATGGACTACGTCGTG	1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCSAGCGTCTCACCTCGAGGGTGAAGGCA	1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
CTGTTTCAGCGTGCTCAACTACGAGCGGGCGCGCGCCCGCCCTCCTGGGCGCCTCTGTG	2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAG	2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC	2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGC	2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG	2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760

FIG. 1C

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGCGGGATTGGCGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	2580 860
GGGCTGCTCCTGCGTTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGCG GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	2640 880
AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	2700 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGT ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	2760 920
CAGATGCCGGCCACGGCCTATTCCCCTGGTGGCGCCTGCTGCTGGATACCCGGACCCTG GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	2820 940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	2880 960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCCGTGCGAACTCTTTGGGGTCTTGGCGCTG AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	2940 980
AAGTGTACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	3000 1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	3060 1020

FIG. 1D

CGTGGG-024130

TTTCATCAGCAAGTTTGAAGAACCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTgatggccaccgcccacagccag	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132
Gccgagagcagacaccagcagccctgtcacgcccggcctctacgtcccagggagggagggg	3480
Cggcccacaccagggcccgaccgctgggagtcctgaggcctgagtgagtggttgccgag	3540
gcctgcatgtccggctgaaggctgagtgccggctgaggcctgagcgagtggtccagccaa	3600
gggctgagtggtccagcacacccgtccgtcttccactccccacaggctggcgctcggtcca	3660
ccccagggccagcttttccctcaccaggagcccggttccactccccacataggaatagtc	3720
catccccagattcgccattgttcacccctcgccctgcccctcctttgccttccacccccac	3780
catccagggtggagaccctgagaaggaccctgggagctctgggaatttgagtgaccaaag	3840
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaatt	3900
ggggggaggtgctgtgggagtaaaatactgaatatatgagtttttcagttttgaaaaaaa	3960
aaaa	3964

FIG. 1E

[illegible]

FIG. 2

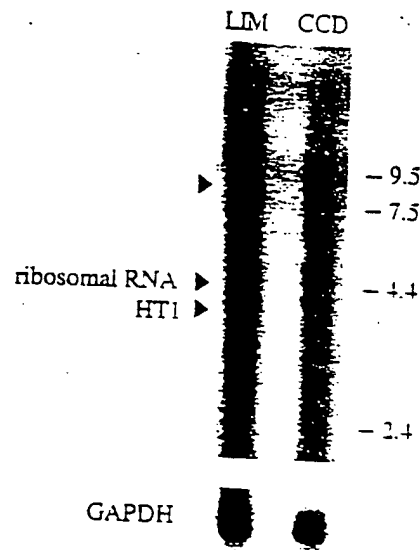


FIG. 3

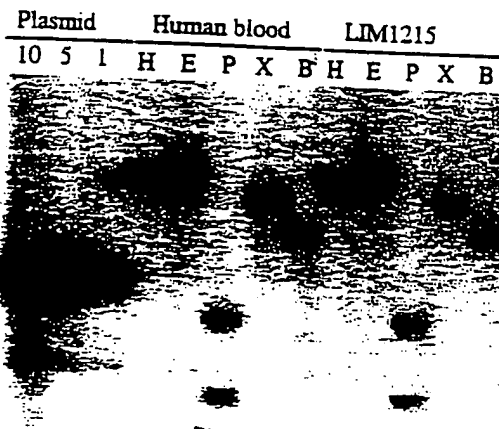


FIG. 4

a b c d e f g h i j k l m n o p

HT1

β -actin

FIG. 5

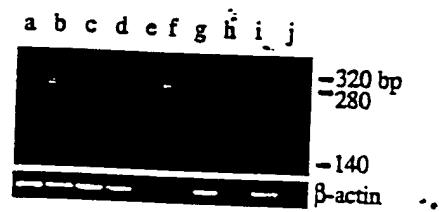


FIG. 6

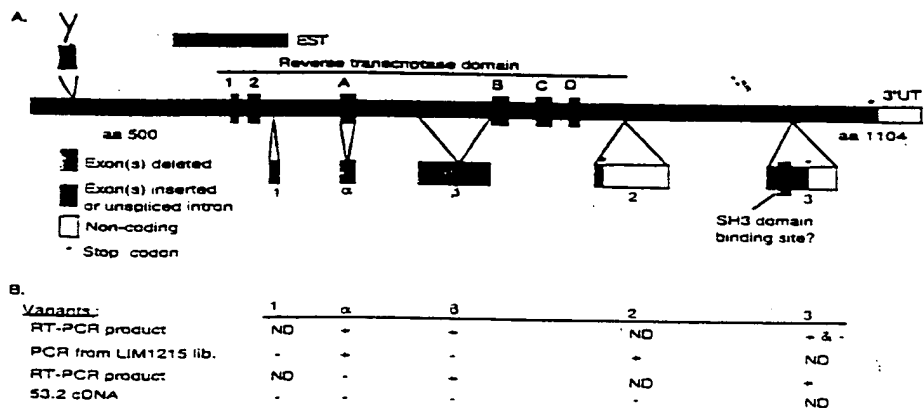


FIG. 7A and 7B

C

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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FIG. 7C

001120-00112050

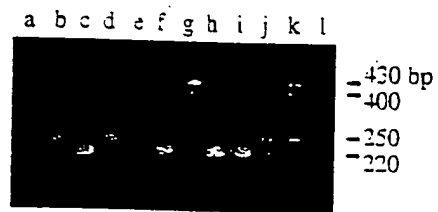


FIG. 8



sequence "γ" 104-105 bases

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTTGGTTTAACTTCCTTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases

GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
Ter

GGCCGTTCGCTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGCCCTCGTCCCATCTGGGGCTGAGCACAATGCATCTTTCTG
TGGGAGTGAGGGTGCCCTCACAACGGGAGCAGTTTCTGTGCTATTTTGGTAA..

sequence "3" 159 bases

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
GlyValGlyLeuGlyLeu *

FIG. 10A

_GACAGTCAACGAGGGGGTGTACCGCCGACTGGGCGTCCCCAGGGTTGACTATAGGA
 CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG
 GTGGACGTGGCCCCGGGCATGGCCTTCTCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
 CACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTGTCTGG
 CTGAGCAAGCCCTCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)

GTGGCTGTGCTTTGGTTTAACTTCCTTTTAAACCAAGTGCCTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCAACCATTTTGTGCGCACAGTGAGGTGGCCGAGGTGCCGGTGCTCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

FIG. 10B

[illegible]

FIG. 11A

FIG. 11B

[illegible]

FIG. 11C

Reference protein

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGAC	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGACCCGCGCGCTTTCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGGCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGTCTGCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCGAGTGTCTGACAGGCGTGTGCSAGCGCGCGCGAAGAAGCTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGTGGACGGGGCGCGGGGGCCCCCGAGGCCTTACCACAGCGTGGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCCAACACCGTGACCGACGCACTGCGGGGGAGCGGGGCTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCGAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCGCGCGCGCGCGCACGCTAGTGSACCGCGAAGCGCTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
CGGGCTTGAACCATAGCGTCAGGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCCGGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGCGCGCGGGCAGTGCAGCGGAAGTCTGCGGTTGCCAAGAGGCGCGAGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCGGAGCGGACGCGCGTTGGGCGAGGCTCTGCGCGCACCGGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGCCTGGTTCCTGTGTGGTGTACCTGCCAGACCGCGCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCACTCCCACTCATCCGTGGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCGCGCGCGCGCGCATCCACATCGCGCGCACACCTCCCTGGGACACGCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCGCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCGCTCCTTCTACTCAGCTCTCTGAGGCGCAGCGCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGGACTCCCGCAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCGCGTGTCTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGGCGCTACGCGGTGCTCCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAAC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420

FIG. 11D

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CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGCTGCCTTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGTTTCGTGCGGCTGCCTGCGCGGCTGGTCCCCCAGGCTCTGGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGCTGCGCTTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
CGCAGGAGCCCCAGGGTTGGCTGTGTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC	1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC	1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
TTTTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTC	1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGGAG	1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
CTGTCCGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCTGCTGACGTCCAGA	1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
CTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATTGTGAACATGGACTACGTCTGTG	1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCACCTCAGGGTGAAGGCA	1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
CTGTTACGGTGTCTCAACTACGAGCGGGCGCGCGCCCCGGCTCTGGGCGCTCTGTG	2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
CTGGGCTGGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAG	2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
GACCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC	2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACAGTACTGC	2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
GTGCGTCGGTATGCGTGGTCCAGAAGCGCGCCATGGGCACGTCCGCAAGGCTTCAAG	2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
AGCCACGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCTGGCTCACCTG	2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTATCGAGCAGAGCTCCTCCCTGAATGAG	2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	800
GCCAGCAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCCACACGCCCTGGCGCATC	2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG	2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGCGGGATTCCGGCGGAC	2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGG	2640

FIG. 11E

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GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCACGGCCTATTCCCTGGTGGCCTGCTGCTGGATACCCGGACCCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGCGGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGTTTCACGCATGTGTGCTGCAGTCCCA	3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGAGGGATGTGCTGGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

FIG. 11F

FIG. 11G

[illegible]

FIG. 11I

ed protein that lacks me . A

[illegible]

FIG. 11J

[illegible]

FIG. 11K

[illegible]

FIG. 11L

truncated protein 1 (ver. 1.0)

[illegible]

FIG. 11M

[illegible]

FIG. 11N

ATGCCGCGGCTCCCGCTGCCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG 60
 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 GTGCTGCCGCTGCCACGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGAC 120
 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
 CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGG 180
 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
 GACGCACGGCCGCCCGCCCGCCCGCCCTCTCCGCCAGGTG
 AspAlaArgProProProAlaAlaProSerPheArgGlnVal
 GGCCTCCCGGGGTCCGCTCCGCTGGGTTGAGGGCGGCTGGGGGAACAGCGACATCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCGCCAGGTG
 G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R P P R R
 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
 TCCTGCCTGAAGGAGCTG 240
 SerCysLeuLysGluLeu 80
 GTGGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCCTTCGGC 300
 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
 TTCGCGCTGTGGACGGGGCCCGCGGGGGCCCCCGGAGGCTTCACACAGCGTGCSC 360
 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
 AGCTACCTGCCCAACACGGTGACCGACGCACTGC3GGGGAGCGGGCTGGGGGCTGCTG 420
 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140
 TTGCGCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCAGCTGC3GCTCTTTGTG 480
 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 CTGGTGGCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGCTCGGCGCT 540
 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 GCCACTCAGGCCCCCGCCCCACACGCTAGTGGACCTCGAAGCGCTCTGGGATGCCAA 600
 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 CGGGCTGGAAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTTGCAGCCCCGGGT 660
 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 GCGAGGAGGCGCGGGGCGAGTGCCAGCCGAAGTCTGCGCTTGGCCAGAGGCGGAGCGT 720
 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 GCGCTGCCCTGAGCCGAGCGGACGCGCTTGGGAGGGGTCTCTGGCCCCACCGGGC 780
 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
 AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCGCGCAA 840
 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGC 900
 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 CGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCGCTCCCTGGGACACGCT 960
 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
 TGTCCCCCGGTGACGCGAGACCAAGCACTTCTCTACTCTCTAGGCGACAAGGAGCAG 1020
 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
 CTGCGGCGCTCTCTCTACTCAGCTCTCTGAGGCGCGAGCTGACTGGCCTCGGAGGCTC 1080
 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 GTGGAGACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGCACTCCCGCAGGTTGCC 1140
 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 CGCTGCCCCAGCGCTACTGGCAATGCGGCGCTGTCTCTGGAGCTGCTTGGGAACAC 1200

FIG. 110

ASU	suPheLeuGluLeuLeuGlyAsnHis	4
	GCGCAGTGGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCC	1260
	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
	CCAGCAGCCGGTGTCTGTGCCCGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG	1320
	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
	GAGGACACAGACCCCGTCCGCTGGTGCACTGCTCCGCCAGCACAGCCCCCTGGCAG	1380
	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
	GTGTACGGCTTCGTGGGGCTGCCCTGCCCGGCTGGTCCCCAGGCTCTGGGGCTCC	1440
	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
	AGGCACAACGAACCGCTTCTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1500
	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
	GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCTGCGGGCTGCGCTTGGCTG	1560
	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
	CGCAGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC	1620
	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
	CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTC	1680
	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
	TTTTATGTACGGAGACCACTTTCAAAGAAGAGGCTCTTTTCTACCGGAAGAGTGTG	1740
	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
	TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCACTGCGGGAG	1800
	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
	CTGTCCGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGA	1860
	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
	CTCCGCTTCATCCCCAAGCCTGACGGGCTGCCGGGATTGTGAACATGGACTACGTGCTG	1920
	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
	GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCA	1980
	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
	CTGTTACGGCTGCTCAACTACGAGCGGGCGGGCGGGCGGGCTCTGGGCGCTCTGTG	2040
	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
	CTGGGCTGGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAG	2100
	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
	GACCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCATC	2160
	AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
	CCCCAGGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCAGAACACGTACTGC	2220
	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
	GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCTTCAAG	2280
	ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
	AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCACAGTTCGTGGCTCACCTG	2340
	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
	CAGGAGACCAGCCCGTGAAGGATGCCCTCCTCATCGAGCAGAGCTCCTCCCTGAATGAG	2400
	GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	800
	GCCAGCAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCGTGCGCATC	2460
	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
	AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG	2520
	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
	CTCTGCAGCCTGTGTACGGCGACATGGAGAACAAGCTGTTTGGGGGATTCCGGCGGAC	2580

FIG. 11P

GGGCTGCTCCTGCGTTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGG	2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACTTCCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCACGGCCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940
GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCCTGTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA	3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAGAACGAGGGATGTGCTGGGGCCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCGGCGCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

FIG. 11Q

[illegible]

FIG. 11R

[illegible]

FIG. 11S

[illegible]

FIG. 11T

AACTACTGATATATATCAGTTTTTCAGTTTTCA

ATGCTTGTGACACAGGCGGAGGACCTGCACCTGGATGGGCTCCCTGTGG...AAATTTGGGGGAGGTGCTGTGGGAGTAA

00500493:004100

FIG. 11U

rotein that lacks motif . ver. 2).

[illegible]

FIG. 11V

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIG. 11W

00120-6610360



FIG. 12

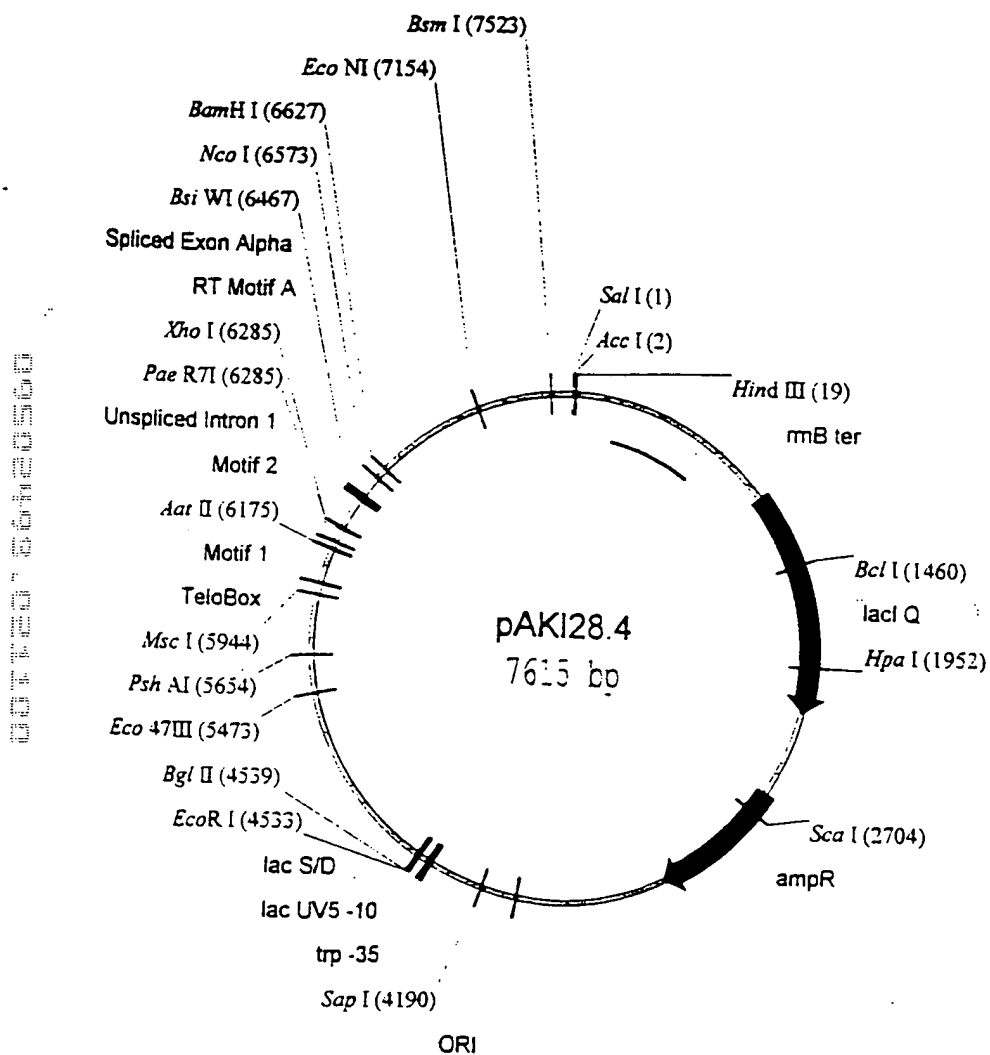


FIG. 13A

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LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

00502490.001400

```
1  tcgacctgca  ggcattgcaag  cttggcactg  gccgtcgttt  tacaacgtcg  tgactgggaa
61  aaccctggcg  ttaccctaact  taatcgccct  gcagcacatc  cccctttcgc  cagctggcgt
121  aatagcgaag  aggcccgcac  cgatcgccct  tcccaacagt  tgcgcagcct  gaatggcgaa
181  tggcgccctga  tgcgggtatct  tctccttacg  catctgtgcg  gtatttcaca  ccgcataaat
241  tccctgtttt  ggcggatgag  agaagatttt  cagcctgata  cagattaaat  cagaacgcag
301  aagcggctctg  ataaaacaga  atttgccttg  cggcagtagc  gcggtgggtc  cacctgaccc
361  catgccgaac  tcagaagtga  aacgccgtag  cggcagtggt  agtgtggggt  ctccccatgc
421  gagagtaggg  aactgccagg  catcaaataa  aacgaaaggc  tcagtcgaaa  gactgggcct
481  ttcgttttat  ctgttggttg  tcggtgaacg  ctctcctgag  taggacaaat  ccgccgggag
541  cggatttgaa  cgttgcgaa  caacggcccc  gaggggtggc  ggcaggacgc  ccgccataaa
601  ctgccaggca  tcaaattaag  cagaaggcca  tcctgacgga  tggccttttt  gcgtttctac
661  aaactcttcc  tgcgttcata  tctacaagcc  atccccccac  agatacggta  aactagcctc
721  gtttttgcat  caggaaaagca  gggaatttat  ggtgcactct  cagtacaatc  tgctctgatg
781  ccgcatagtt  aagccagccc  cgacacccgc  caacacccgc  tgacgcgccc  tgacgggctt
```

FIG. 13B

841 gtctgtctccc ggcattccgct tacagacaag ctgtgaccgt ctccggggagc tgcattgtgtc
901 agagggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctctgtg ataccgcctat
961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccattcgaatg gtgcaaaacc tttcgcggtg tggcatgata gcgcccgga gagagtcaat
1081 tcagggtggt gaatgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccggt gtggtgaacc aggccagcca cgtttctgtc ggcagcggtg
1201 aaaaagtggg agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcggggcaa acagtctgtg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcgaat tgtcgcggcg attaaatctc gcgcgatca actgggtgccc agcgtggtg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaaagc ggcgggtgcac aatctctctg
1441 cgcaacgcgt cagtgggctg atcatttaact atccgctgga tgaccaggat gccattgtctg
1501 tgggaagctgc ctgcaactat gtcccgcggt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtgat tatttctctc catgaagacg gtacgcgact gggcgtggag cactctggtcg
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1981 tggggcaaac cagcgtggac cgttctgtgc aactctctca gggccagcggt gtgaagggca
2041 atcagctgtt gcccgctctca ctggctgaaaa gaaaaaccac cctggcgccc aatacgcaaa
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2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagt agctccactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggttg cactttctgg
2281 ggaatgtgc gcggaacccc tatctgttta ttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataaccttg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttatctcc tttttcggc catcttgccc tctgtctctt
2461 gccacccag aaacgcctgt gaaagtataa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacctg agaactggat ctcaacagcg gtaagattct tgagagttct cgcgccgaag
2581 aacgtttctc aatgatgagc acttttaaa tctgtctatg tggcgcggtg tctatccgta
2641 ttgacgcgg gcaagagcaa ctccgctgccc gcatacacta tttcagaaat gacttggctg
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2761 gtgctgccat aacctgagt gataacactg cggccaactt actctgaca acgatcggag
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2981 gttgggaacc ggaactgaa gaaacctatc caaacgacga gcgtgacac accgatgcctg
2941 tagcaatggc aacaacgttg cgcgaactat taactggcga actacttact ctagcttccc
3001 ggcacaacat aatagactgg atggagcgcg ataaagtggc aggaccactt ctgcgctcgg
3061 cctttccggc tggctggctt attgtgata aatctggagc cgttgagcgt gggctctcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tctcgtagt atctacacga
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4081 tttctgctt atccccgat tctgttgata accgtattac cgccttctgag tgagctgata
4141 ccgctcgcg cagcgaacg accgagcgca gcgagtcagt gagcggaggaa gcggaagagc
4201 gcccaatcag caaacggctt cttcccgccc gtcggccgat tcaatcaatgc agaatttaatt

FIG. 13C

FIG. 13D

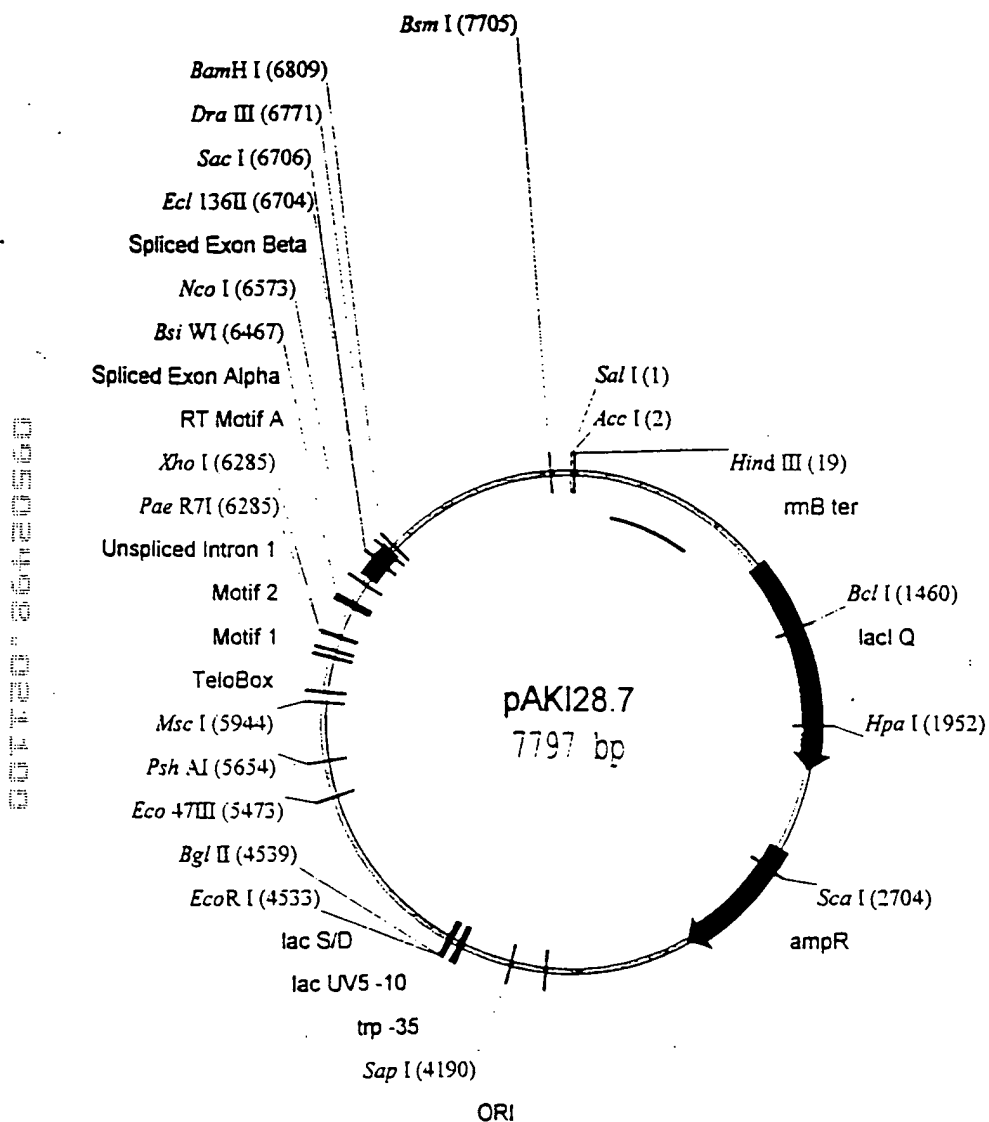


FIG. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

```

1   tcgacctgca ggcattgcaag cttggcactg gccctcgctt tacaacgtcg tgactgggaa
61  aaccttgggc ttaccaact taatcgccct gcagcacatc cccctttcgc cagctggcgt
121 aatagcggaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
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361 catgccgaac tcagaagtga aacgccgtag cgcgcatggt agtgtggggg ctccccatgc
421 gagagtaggg aactgccagg catcaataa aacgaaaggc tcagtgcgaa gactgggcct
481 ttcgttttat ctgttgtttg tcggtgaacg ctctcctgag taggacaaat ccgcggggag

```

FIG. 14B

FIG. 14C

3961 tctgacttga gcgtcgatct tctgtatgct cgtcaggggg ggggagccta tggaaaaacg
4021 ccagcaacgc ggcctcttcta cggctctctgg ccttttctgt gccttttctt cactatgtctt
4081 ttctctcgctt atccccctgat tctgtggata accgtattac cgcctttgag tgagctgata
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4201 gcccaatacg caaacgcctt cctcccgcgc gttggccgat tcattaatgc agaattaatt
4261 ctcattgtttg acagcttatt atcgacttga cgggtgcacca atgtcttctgg cgtcaggcag
4321 ccacgggaag ctgtggtatg gctgtgcagg tctgaaatca ctgcataatt cgtgtcgcct
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4441 tattctgaaa tgagctgttg acaatttatt atcggtctgt ataattgttg gaattgtgag
4501 cggataacaa ttccacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
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4621 tgcgctgctt ggacggggcc cgcggggggc cccccaggc cttcaccacc agcgtgcgca
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4801 tgggtggcttc cagctgcgcct taccagggtg gcggcgcgcc gctgtaccag ctcggcgctg
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5041 gcgctgcccc tgagccggag cggacgcccc ttgggcaggg gtcttggggc cccccgggca
5101 ggacgctgtg accgagtgac cgtgggtttt gtgtgtgtgt accctggcga ccccgcggaag
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5221 gccagcaccg cggcgggccc ccatccacat cggcgccacc acgtccctgg gacacgctt
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6841 tctgcagcct gtgtacgac gacatggaga acaagctgtt tgcggggatt cggcgggagc
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6961 aaactctctt aggacctgtt ccgaagtgtt ctgagtatgt ctgctggtg aacttgcgga
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7081 tggcgcccca cggcctatct ccttgggtgt gcttctgtgt ggatacccg accctggagg
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7261 gtcacagcct gttcttggat ttgcaggtga acagcctcca gacggtgtgc accaactct
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FIG. 14D

[illegible]

FIG. 14E

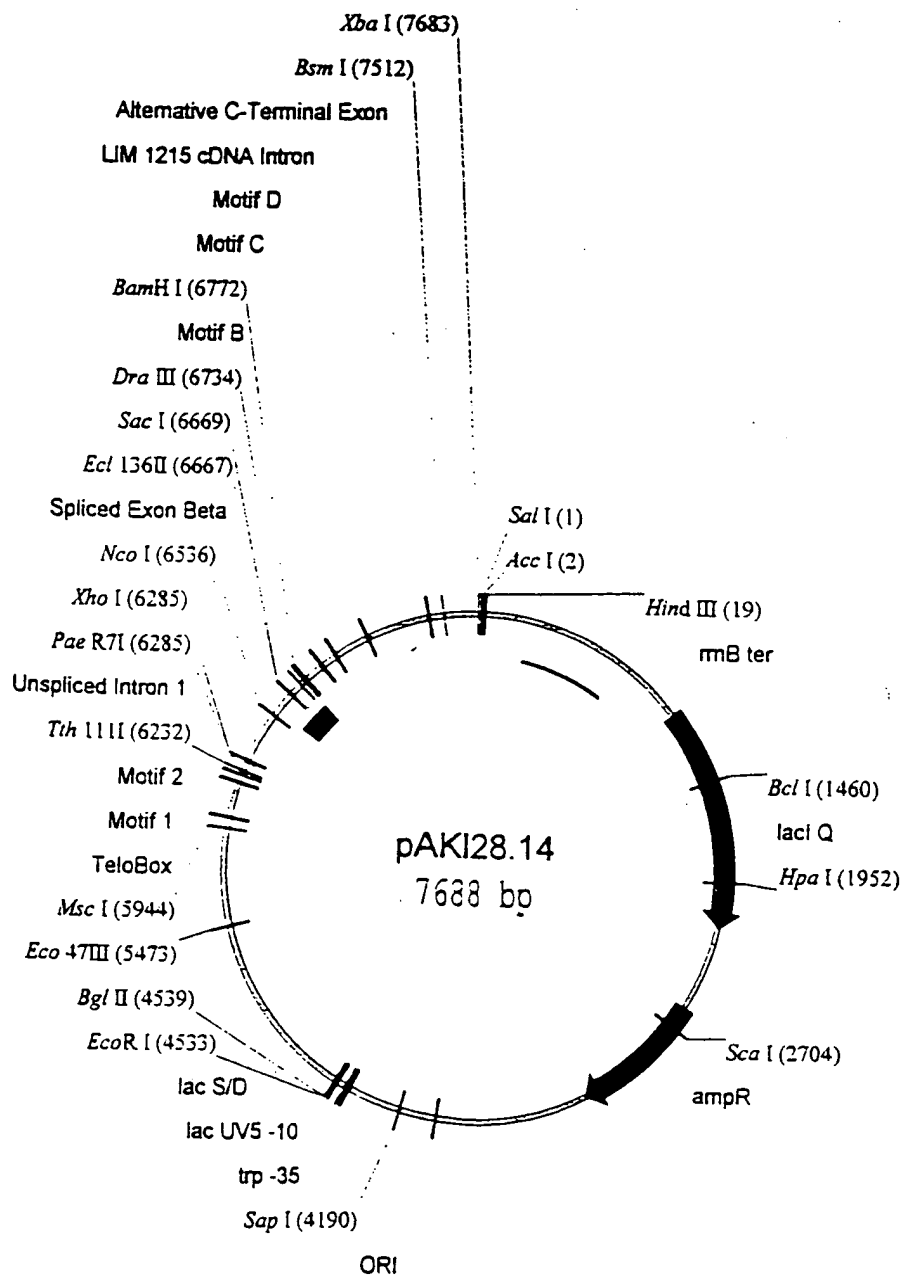


FIG. 15A

PRINT OF DRAWINGS
AS ORIGINALLY FILED

LOCUS PAK129.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

1 tcgacctgca ggcatgcaag cttggcactg gccgtcgttt tacaacgtcg tgactgggaa
61 aacctggcgg ttaccaact taatcgctt gcagcacatc cccctttcgc cagctggcgt
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661 aaactcttcc tgtcgtcata tctacaagcc atccccccac agatacggta aactagcctc
721 gtttttgcac caggaaagca gggaatttat ggtgcactct cagtacaaat tgctctgatg
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FIG. 15B

CGC01100.01400

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3481 cgctaccagc ggtggtttgt ttgcccagtc aagagctacc aactcttttt ccgaaggtaa
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4921 gggccctgaa ccatagcgtt agggagggcg gggctccccc gggcctgcca gcccccggctg
4981 cgaggagggc cggggggcag gccagccgaa gtctgcccgt gcccaagagg cccaggcgctg
5041 gcgctgcccc tgagcgggag cggacgcccc ttgggcaggg gtccctgggc cccccgggca
5101 ggacgctgtg accgagctgac cgtgtgtttt gtgtgtgttc acctgccaga cccgcccga
5161 aagccacctt tttggagggt ggcctctctg gcacgcgcca ctcccacca tccgtgggct
5221 gccagcacea cgcggggccc ccatccacat cggcgccacc acgtccctgg gacacgctt
5281 gtcccccggt gtacgcccag accaagcact tctctactc ctcaggcgag aaggagcagc
5341 tgcggccctc cttctacttc agctctctga ggcaccagcc gactcgcgct cggaggtctg
5401 tggagaccat cttctgtggg tccagggccc ggaatgccag gactccccgc aggtcgcccc
5461 gccctgcccc gcgtactgtg caaatgtggc cctctgtctt ggagctgctt gggaaaccag
5521 cgcagtgccc ctacgggggt ctcccgaaga cgcactgccc gctgcgagct gcggccacc
5581 cagcagccgg tgtctgtgct cggggaagac cccagggctc tgtggcgggc cccgagggag
5641 aggacacaga ccccccgtgc ctgtgtcagc tgcctcgcca gcacagcagc cctggcgagg
5701 tgtacggctt cgtgcggggc tgcctgcgct ggcctggctc cccagggctc tggggctcca
5761 ggcacaacga accgcccctt ctcagggaaca ccaagaagt catctccctg gggaaagcatg
5821 ccaagctctc gctgcaggag ctgacgttga agatgagcgt gcgggactgc gcttggctgc
5881 gcaggagccc aggggttgcc tgtgtctcgg ccgcagagca cctgtctgct gaggagatcc
5941 tggccaagt cctgcactgg ctgtatgagt tgtacgtcgt cgagctgctc aggtctctct
6001 tttatgtcac ggaagccacg tttccaaaaga acaggctctt tttctaccgg aagagtgtct
6061 ggaagcaagt gcaaaagcat ggaattagac agcacttgaa gaggtgagc ctgcgggagc
6121 tgtcggaagc agaggttagg cagcatctgg aagccaggcc cgccctgctg acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggcgattgt gaacatggac tacgtcgtgg
6241 gagccagaac gttccgcaga gaaaagagg ccgagcgtct cacttcgagg gtgaaggcac
6301 tgttcagcgt gctcaactac gagcggcgct ggcgcccgg cctccctggc gcctctgtgc
6361 tgggcttggg cgatatccac agggctctgc gcacctctg gctgcgtgtg cggggccagg
6421 acccgccgct tgagctgtac tttgtcaagg acaggctcac ggaaggtcat gccagcatca
6481 tcaaacccag aacacgtact gcgtgcgtct gtatgcgctg gtccagaagg ccgccatgg
6541 gcacgtccgc aaggccttca agagccactc cttacctg acagacctcc agcgtacat
6601 gcagacgttc gtggctcacc tgcaggagac cagcccgctg agggatgctg tctcatcga
6661 gcagagctcc tccctgaatg aggcagcag tggcctcttc gacgtctctc tacgtctcat
6721 gtgccaccac gccgtgcgca tcaagggcaa gtctacgtc cagtgcagg ggaatccgca

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FIG. 15C

6781 gggtccatc ctctccacgc tgctctgcag cctgtgctac ggcgacatgg agaacaagct
6841 gtttgcgggg attcggcggg acgggctgct cctgcgtttg gtggatgatt tcttggtggg
6901 gacacctcac ctcacccacg cgaaaacctt cctcaggacc ctgggtccgag gtgtccctga
6961 gtatggctgc gtggtgaact tgcggaagac agtgggtgaac ttccctgtag aagacgaggc
7021 cctgggtggc acggcttttg ttcagatgcc ggcccacggc ctattcccct ggtgcggcct
7081 gctgctggat acccgaccc tggagggtgca gacgactac tccagctatg cccggacctc
7141 catcagagcc agtctcacct tcaaccgcgg cttcaaggct gggaggaaca tgcgtcgcaa
7201 actctttggg gtcttgcggc tgaagtgtca cagcctgtt ctggatttgc aggtgaacag
7261 cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acaggtttca
7321 cgcatgtgtg ctgcagctcc catttcatca gcaagtttg aagaaccca cattttcct
7381 gcggtcatc tctgacacgg cctcccctg ctactccatc ctgaaagcca agaacgcagg
7441 gatgtcgctg ggggccaagg gcgcgcggc cctctgccc tccgaggccg tgcagtggct
7501 gtgccaccaa gcattcctgc tcaagctgac tcgacaccgt gtcacctacg tgccactcct
7561 ggggtcactc aggacagccc agacgcagct gagtcggaag ctcccgggga cgacgtgac
7621 tgccctggag gccgcagcca acccggcact gccctcagac ttcaagacca tcctggactg
7681 atctagag

CGCCTGAG

FIG. 15D